SCORE Search Results Details for Application 10552515 and Search Result 20080630_144055_us-10-552-515-5.rag.

This page gives you Search Results detail for the Application 10552515 and Search Result 20080630_144055_us-10-552-515-5.rag.

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GenCore version 6.2.1

OM protein - protein search, using sw model

Run on: June 30, 2008, 17:43:01 ; Search time 71 Seconds
(without alignments)
76.429 Million cell updates/sec

Title: US-10-552-515-5
Perfect score: 43
Sequence: 1 ALLSASWAV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3405708 seqs, 601879884 residues

Total number of hits satisfying chosen parameters: 3405708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200711:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000:*
4: geneseqp2001:*
5: geneseqp2002:*
6: geneseqp2003a:*
7: geneseqp2003b:*
8: geneseqp2004a:*

9: geneseqp2004b:*
10: geneseqp2005:*
11: geneseqp2006:*
12: geneseqp2007:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	100.0	9	8	ADT77668	Adt77668 Splice va
2	43	100.0	843	10	AEB13424	Aeb13424 Human pro
3	43	100.0	885	10	AEB13426	Aeb13426 Human pro
4	43	100.0	898	4	ABG15488	Abg15488 Novel hum
5	43	100.0	933	8	ADT77664	Adt77664 Splice va
6	43	100.0	933	11	AEL84788	Ael84788 Tumor mar
7	40	93.0	84	5	ABJ01075	Abj01075 Ovary cel
8	38	88.4	113	4	AAB79567	Aab79567 Corynebac
9	38	88.4	264	4	AAG90241	Aag90241 C glutami
10	36	83.7	763	10	AEN26433	Aen26433 Oryza sat
11	36	83.7	869	10	ADW81389	Adw81389 MAP3K9 ge
12	36	83.7	869	11	AEK84872	Aek84872 Human MAP
13	36	83.7	922	8	ADO01052	Ado01052 Human hom
14	36	83.7	1066	10	AEN28397	Aen28397 Homo sapi
15	36	83.7	1071	10	ADW81388	Adw81388 MAP3K9 ge
16	36	83.7	1071	11	AEK84871	Aek84871 Human MAP
17	36	83.7	1096	7	ADE47768	Ade47768 Human NOV
18	36	83.7	1096	8	ADJ79038	Adj79038 Human NOV
19	36	83.7	1118	8	ADM87166	Adm87166 Human pro
20	36	83.7	1118	10	AED24227	Aed24227 Human mit
21	35	81.4	58	4	AAB85074	Aab85074 Human ser
22	35	81.4	100	7	ADF59180	Adf59180 Human pol
23	35	81.4	259	2	AAW60134	Aaw60134 M. vaccae
24	35	81.4	259	2	AAY14881	Aay14881 M. vaccae
25	35	81.4	259	5	ABB73487	Abb73487 M vaccae
26	35	81.4	269	4	AAB84203	Aab84203 Amino aci
27	35	81.4	269	5	ABG31348	Abg31348 Human ser
28	35	81.4	269	6	ABG72908	Abg72908 Novel hum
29	35	81.4	280	5	AAB47910	Aab47910 MASP-like
30	35	81.4	292	8	ABO58361	Abo58361 Human gen
31	35	81.4	319	4	AAM25653	Aam25653 Human pro
32	35	81.4	343	6	ABU99151	Abu99151 Novel hum
33	35	81.4	343	8	ADM93867	Adm93867 Human NOV
34	35	81.4	343	11	AEG57039	Aeg57039 Human NOV
35	35	81.4	728	4	AAB85060	Aab85060 Human ser

36	35	81.4	728	4	AAB47559	Aab47559 Protease
37	35	81.4	728	7	ADE87461	Ade87461 Human MBL
38	35	81.4	728	8	ADL91027	Adl91027 Human man
39	35	81.4	728	12	AFY30852	Afy30852 Human sca
40	35	81.4	728	12	AFY31044	Afy31044 Complemen
41	34	79.1	314	4	ABG26369	Abg26369 Novel hum
42	34	79.1	345	4	AAG90308	Aag90308 C glutami
43	34	79.1	388	10	AED46943	Aed46943 Membrane
44	34	79.1	388	12	AER29459	Aer29459 C. glutam
45	34	79.1	404	8	ADN24647	Adn24647 Bacterial

ALIGNMENTS

RESULT 1
ADT77668
ID ADT77668 standard; peptide; 9 AA.
XX
AC ADT77668;
XX
DT 13-JAN-2005 (first entry)
XX
DE Splice variant-novel gene expressed in prostate (SV-NGEP) epitope.
XX
KW Splice variant-novel gene expressed in prostate; SV-NGEP; human;
KW prostate cancer; cytostatic; gene therapy; immunotherapy; epitope.
XX
OS Homo sapiens.
XX
PN WO2004092213-A1.
XX
PD 28-OCT-2004.
XX
PF 05-APR-2004; 2004WO-US010588.
XX
PR 08-APR-2003; 2003US-0461399P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Pastan I, Bera TK, Lee B;
XX
DR WPI; 2004-758338/74.
XX
PT New Splice Variant-Novel Gene Expressed in Prostate polypeptide or
PT encoding nucleic acid molecule for diagnosing, preventing or treating
PT cancer, especially prostate cancer.
XX
PS Disclosure; SEQ ID NO 5; 88pp; English.

XX
CC The present sequence is that of a predicted epitope of human splice
CC variant-novel gene expressed in prostate (SV-NGEP) ADT77664. The epitope
CC is predicted to bind HLA2-01 and was identified using an HLA binding
CC motif program. It corresponds to amino acids 170-178 of SV-NGEP.
CC Polypeptides comprising an immunogenic fragment of 8 consecutive amino
CC acids of SV-NGEP which specifically bind to an antibody that specifically
CC binds a polypeptide comprising amino acids 157-933 of SV-NGEP are
CC claimed. The invention provides methods for: detecting prostate cancer in
CC a subject by contacting a sample with an antibody that specifically binds
CC a SV-NGEP polypeptide and detecting the formation of an immune complex,
CC or detecting an increase in expression of SV-NGEP polypeptide or mRNA;
CC producing an immune response against a cell expressing SV-NGEP, for
CC example in a subject with prostate cancer, by administering SV-NGEP
CC polypeptide or polynucleotide to produce an immune response that
CC decreases growth of the prostate cancer; inhibiting the growth of a
CC malignant cell that expresses SV-NGEP by culturing cytotoxic T
CC lymphocytes (CTLs) with SV-NGEP to produce activated CTLs, and contacting
CC these with the malignant cell; and inhibiting the growth of a malignant
CC cell by contact with an antibody that specifically binds SV-NGEP, where
CC the antibody is linked to a chemotherapeutic agent or toxin.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 43; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ALLSASWAV 9
              |||||||||
Db          1 ALLSASWAV 9
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RESULT 2
AEB13424
ID AEB13424 standard; protein; 843 AA.
XX
AC AEB13424;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human prostate specific polypeptide #1.
XX
KW Screening; diagnosis; drug delivery; prostate specific polypeptide;
KW cancer; prostate tumor; cytostatic; neoplasm.
XX
OS Homo sapiens.
XX
PN WO2005062788-A2.

XX
PD 14-JUL-2005.
XX
PF 16-DEC-2004; 2004WO-US042406.
XX
PR 22-DEC-2003; 2003US-0531809P.
XX
PA (AVAL-) AVALON PHARM INC.
XX
PI Weigle B, Ebner R;
XX
DR WPI; 2005-497793/50.
DR N-PSDB; AEB13423.
XX
PT Novel isolated prostate specific polypeptide, useful for treating cancer,
PT and identifying agent that modulates activity of cancer related gene.
XX
PS Claim 12; SEQ ID NO 3; 59pp; English.
XX
CC The invention relates to an isolated prostate specific polypeptide
CC comprising one or more immunogenic fragments. The invention also relates
CC to a method of identifying an agent that modulates the activity of a
CC cancer related gene involving contacting a compound with a cell
CC containing a gene under conditions promoting the expression of the gene,
CC detecting a difference in expression of the gene relative to when the
CC compound is not present and identifying an agent that modulates the
CC activity of a cancer related gene, a method of identifying an anti-
CC neoplastic agent involving contacting a cell exhibiting neoplastic
CC activity with a compound first identified as a cancer related gene
CC modulator using and determining a decrease in neoplastic activity after
CC contacting, when compared to when the contacting does not occur, or
CC administering an agent first identified to an animal exhibiting a cancer
CC condition and detecting a decrease in cancerous condition, a method of
CC determining the cancerous status of a cell involving determining an
CC increase in the level of expression in a cell of a gene where an elevated
CC expression relative to a known non-cancerous cell indicates a cancerous
CC state or potentially cancerous state, an antibody that reacts with a
CC prostate specific polypeptide, an immunoconjugate comprising the antibody
CC and a cytotoxic agent, a method of treating cancer involving contacting a
CC cancerous cell in vivo with an agent having activity against a prostate
CC specific polypeptide and an immunogenic composition the prostate specific
CC polypeptide. The prostate specific polypeptide is useful for identifying
CC an agent that modulates the activity of a cancer related gene. The
CC immunogenic composition is useful for treating cancer, preferably
CC prostate cancer in an animal, e.g. human, which involves administering
CC the immunogenic composition that is sufficient to elicit the production
CC of cytotoxic T lymphocytes specific for the prostate specific
CC polypeptide. The invention is useful for identifying anti-neoplastic
CC agents. This sequence represents a human prostate specific polypeptide of

```
CC   the invention.
XX
SQ   Sequence 843 AA;

  Query Match             100.0%;  Score 43;  DB 10;  Length 843;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ALLSASWAV 9
              |||||||||
Db        171 ALLSASWAV 179


RESULT 3
AEB13426
ID   AEB13426 standard; protein; 885 AA.
XX
AC   AEB13426;
XX
DT   22-SEP-2005  (first entry)
XX
DE   Human prostate specific polypeptide #2.
XX
KW   Screening; diagnosis; drug delivery; prostate specific polypeptide;
KW   cancer; prostate tumor; cytostatic; neoplasm.
XX
OS   Homo sapiens.
XX
PN   WO2005062788-A2.
XX
PD   14-JUL-2005.
XX
PF   16-DEC-2004; 2004WO-US042406.
XX
PR   22-DEC-2003; 2003US-0531809P.
XX
PA   (AVAL-) AVALON PHARM INC.
XX
PI   Weigle B,  Ebner R;
XX
DR   WPI; 2005-497793/50.
DR   N-PSDB; AEB13425.
XX
PT   Novel isolated prostate specific polypeptide, useful for treating cancer,
PT   and identifying agent that modulates activity of cancer related gene.
XX
PS   Claim 12; SEQ ID NO 5; 59pp; English.
XX
CC   The invention relates to an isolated prostate specific polypeptide
```

CC comprising one or more immunogenic fragments. The invention also relates
CC to a method of identifying an agent that modulates the activity of a
CC cancer related gene involving contacting a compound with a cell
CC containing a gene under conditions promoting the expression of the gene,
CC detecting a difference in expression of the gene relative to when the
CC compound is not present and identifying an agent that modulates the
CC activity of a cancer related gene, a method of identifying an anti-
CC neoplastic agent involving contacting a cell exhibiting neoplastic
CC activity with a compound first identified as a cancer related gene
CC modulator using and determining a decrease in neoplastic activity after
CC contacting, when compared to when the contacting does not occur, or
CC administering an agent first identified to an animal exhibiting a cancer
CC condition and detecting a decrease in cancerous condition, a method of
CC determining the cancerous status of a cell involving determining an
CC increase in the level of expression in a cell of a gene where an elevated
CC expression relative to a known non-cancerous cell indicates a cancerous
CC state or potentially cancerous state, an antibody that reacts with a
CC prostate specific polypeptide, an immunoconjugate comprising the antibody
CC and a cytotoxic agent, a method of treating cancer involving contacting a
CC cancerous cell in vivo with an agent having activity against a prostate
CC specific polypeptide and an immunogenic composition the prostate specific
CC polypeptide. The prostate specific polypeptide is useful for identifying
CC an agent that modulates the activity of a cancer related gene. The
CC immunogenic composition is useful for treating cancer, preferably
CC prostate cancer in an animal, e.g. human, which involves administering
CC the immunogenic composition that is sufficient to elicit the production
CC of cytotoxic T lymphocytes specific for the prostate specific
CC polypeptide. The invention is useful for identifying anti-neoplastic
CC agents. This sequence represents a human prostate specific polypeptide of
CC the invention.
XX
SQ Sequence 885 AA;

Query Match 100.0%; Score 43; DB 10; Length 885;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ALLSASWAV 9
              |||||||||
Db        171 ALLSASWAV 179
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RESULT 4
ABG15488
ID ABG15488 standard; protein; 898 AA.
XX
AC ABG15488;
XX
DT 18-FEB-2002 (first entry)

XX
DE Novel human diagnostic protein #15479.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS79675.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 45847; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this

```
CC   patent did not appear in the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 898 AA;

  Query Match             100.0%;  Score 43;  DB 4;  Length 898;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ALLSASWAV 9
              |||||||||
Db        263 ALLSASWAV 271


RESULT 5
ADT77664
ID   ADT77664 standard; protein; 933 AA.
XX
AC   ADT77664;
XX
DT   15-JUN-2007  (revised)
DT   13-JAN-2005  (first entry)
XX
DE   Splice variant-novel gene expressed in prostate (SV-NGEP) polypeptide.
XX
KW   Splice variant-novel gene expressed in prostate; SV-NGEP; human;
KW   prostate cancer; cytostatic; gene therapy; immunotherapy; BOND_PC;
KW   NGEP long variant; NGEP long variant [Homo sapiens]; GO5886.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          1. .345
FT                   /label= Cytoplasmic
FT   Region          157. .933
FT                   /note= "An immunogenic fragment comprising 8 consecutive
FT                   amino acids that specifically binds to an antibody that
FT                   specifixally binds to a polypeptide comprising amino
FT                   acids 157-933 is referred to in Claim 1"
FT   Region          170. .178
FT                   /note= "Epitope, predicted to bind HLA2-01"
FT   Region          215. .223
FT                   /note= "Epitope, predicted to bind HLA2-01"
FT   Region          258. .266
FT                   /note= "Epitope, predicted to bind HLA2-01"
FT   Domain          346. .368
FT                   /label= Transmembrane
FT   Domain          369. .421
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FT                   /label= External
FT                   /note= "Cell surface"
FT   Region          403. .411
FT                   /note= "Epitope, predicted to bind HLA2-01"
FT   Domain          422. .441
FT                   /label= Transmembrane
FT   Region          427. .435
FT                   /note= "Epitope, predicted to bind HLA2-01"
FT   Domain          442. .501
FT                   /label= Cytoplasmic
FT   Domain          502. .524
FT                   /label= Transmembrane
FT   Domain          525. .543
FT                   /label= External
FT                   /note= "Cell surface"
FT   Domain          544. .566
FT                   /label= Transmembrane
FT   Region          557. .565
FT                   /note= "Epitope, predicted to bind HLA2-01"
FT   Region          562. .570
FT                   /note= "Epitope, predicted to bind HLA2-01"
FT   Domain          567. .586
FT                   /label= Cytoplasmic
FT   Domain          587. .609
FT                   /label= Transmembrane
FT   Domain          610. .714
FT                   /label= External
FT                   /note= "Cell surface"
FT   Domain          715. .737
FT                   /label= Transmembrane
FT   Domain          738. .761
FT                   /label= Cytoplasmic
FT   Domain          762. .784
FT                   /label= Transmembrane
FT   Domain          785. .933
FT                   /label= External
FT                   /note= "Cell surface"
FT   Region          846. .854
FT                   /note= "Epitope, predicted to bind HLA2-01"
XX
PN   WO2004092213-A1.
XX
PD   28-OCT-2004.
XX
PF   05-APR-2004; 2004WO-US010588.
XX
PR   08-APR-2003; 2003US-0461399P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
```

XX
PI Pastan I, Bera TK, Lee B;
XX
DR WPI; 2004-758338/74.
DR N-PSDB; ADT77665.
DR PC:NCBI; gi48093524.
XX
PT New Splice Variant-Novel Gene Expressed in Prostate polypeptide or
PT encoding nucleic acid molecule for diagnosing, preventing or treating
PT cancer, especially prostate cancer.
XX
PS Claim 1; SEQ ID NO 1; 88pp; English.
XX
CC The present sequence is the protein sequence of splice variant-novel gene
CC expressed in prostate (SV-NGEP). SV-NGEP is identical to NGEP from amino
CC acid 1-157, diverging from amino acid 158. Expression analysis in 76
CC normal and foetal tissues showed SV-NGEP to be strongly expressed only in
CC a prostate sample. Claimed methods for detecting prostate cancer in a
CC subject comprise: contacting the sample with an antibody that
CC specifically binds a SV-NGEP polypeptide and detecting the formation of
CC an immune complex; or detecting an increase in expression of SV-NGEP
CC polypeptide or mRNA. Antibodies to an SV-NGEP polypeptide can be used to
CC detect metastatic prostate cancer cells at locations other than the
CC prostate. A claimed method for producing an immune response against a
CC cell expressing SV-NGEP, for example in a subject with prostate cancer,
CC comprises administering the polypeptide, or a polynucleotide encoding it,
CC to produce an immune response that decreases growth of the prostate
CC cancer. A claimed method for inhibiting the growth of a malignant cell
CC that expresses SV-NGEP comprises culturing cytotoxic T lymphocytes (CTLs)
CC with SV-NGEP to produce activated CTLs that recognise an NGEP expressing
CC cell, and contacting the malignant cell with the activated CTLs.
CC Alternatively, growth of a malignant cell is inhibited by contact with an
CC antibody that specifically binds an SV-NGEP polypeptide, where the
CC antibody is linked to an effector molecule (chemotherapeutic agent or
CC toxin) that inhibits growth of the malignant cell. This may be performed
CC in vivo. Kits for detecting an SV-NGEP polypeptide or polynucleotide in a
CC sample are also claimed.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 933 AA;

Query Match 100.0%; Score 43; DB 8; Length 933;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALLSASWAV 9
|||||||||

Db 170 ALLSASWAV 178

RESULT 6
AEL84788
ID AEL84788 standard; protein; 933 AA.
XX
AC AEL84788;
XX
DT 18-OCT-2007 (revised)
DT 15-JUN-2007 (revised)
DT 28-DEC-2006 (first entry)
XX
DE Tumor marker gene NGEP SEQ ID NO 155.
XX
KW cytostatic; diagnosis; prognosis; tumor marker; gene expression;
KW drug screening; cancer; neoplasm; NGEP; BOND_PC; NGEP long variant;
KW GO5886.
XX
OS Homo sapiens.
XX
PN WO2006110593-A2.
XX
PD 19-OCT-2006.
XX
PF 07-APR-2006; 2006WO-US013172.
XX
PR 07-APR-2005; 2005US-0669342P.
PR 11-OCT-2005; 2005US-0725982P.
XX
PA (MACR-) MACROGENICS INC.
XX
PI Von Haller PD, Schummer M, Meyer DW, Schubert LA, Tjoelker LW;
XX
DR WPI; 2006-814687/82.
DR N-PSDB; AEL84787.
DR REFSEQ; NP_001001891.
DR PC:NCBI; gi48093524.
XX
PT Detecting or diagnosing cancer in a subject comprises determining
PT expression of at least one gene, and comparing level of expression to a
PT control sample from a normal subject, where increased expression level
PT indicates cancer.
XX
PS Claim 8; SEQ ID NO 155; 583pp; English.
XX
CC The invention describes a method of detecting or diagnosing cancer in a
CC subject comprising determining the expression level of at least one gene,
CC and comparing the level of expression to a corresponding control sample

CC from a normal subject, where cancer is detected or diagnosed if there is
CC an increase in the expression level of the gene relative to the
CC expression in the control sample. Also described are: identifying a
CC compound to be tested for its ability to prevent, treat, manage, or
CC ameliorate cancer or its symptom; a compound identified by the method;
CC treating cancer in a patient; treating a cancer in a subject that is
CC fully or partially refractory to a first treatment in a patient; and a
CC pharmaceutical composition comprising an amount of an antibody selected
CC from anti-SLC12A2, anti-FLJ23375, anti-GRM5, anti-TAS2R1, anti-NRXN2,
CC anti-C14orf160, anti-MGC 15668, anti-MGC33486, anti-TMEM16F, anti-FAT,
CC anti-KIAA0195, anti-LRFN, anti-NFASC, anti-BAT2D1, anti-MGC2963, anti-
CC KIAA0685, anti-EDG3, anti-GGTL3, anti-PLVAP, anti-FLJ31528, anti-
CC FLJ90709, anti-VEZATIN, anti-TMPRSS9, anti-ATP13A5, anti-PKHD1L1, anti-
CC C2orf18, anti-ANKRD22, anti-FAM62B, anti-LOC57168, anti-CDKAL1, anti-
CC SLC39A3v1, anti-SLC39A3v2, anti-BAT5, anti-TM9SF4, anti-DC2, anti-VAPB,
CC anti-XTP3TPB, anti-TACSTD2, anti-FNDC3A, anti-GK001, anti-OCIAD2, anti-
CC PR01855, anti-C20orf3, anti-SDFR1, anti-FLJ20481, anti-LENG4, anti-
CC FLJ12443, anti-ARP5 Long, anti-ARP5 Short, anti-TMD0645, anti-NGEP, anti-
CC IL1RAP1, anti-PLXNB1, anti-ATP2B2, anti~FLJ11848, anti-ENTPD2, anti-
CC PPM1H, anti-KRTKAP3, anti-KCNC3, anti-TM9SF1, anti-ULBP1, anti-C19orf26,
CC anti-KIAA830, anti-KIAA1244, anti-KIAA1797, anti-MGC26856, anti-NETO2,
CC anti-SUSD2, anti-FOLR2, anti-EMR2, ENTPD1, anti-ATP10B, anti-PTK7, anti-
CC FLJ14681, anti-C20orf22, anti-FLJ14281, anti-FAM8A1, anti-TMED7, anti-
CC C20orf108, anti-ATAD1, anti-GPR154, anti-C14orf27, anti-OSAP, anti-
CC FAD104, anti-FLJ90492, anti-SLC27A3, anti-RON, anti-ATP13A1, anti-
CC DKFZP564D166, anti-ESSPL, anti-EXTL3, anti-KAI1, anti-KIAA0960, anti-
CC MTRNL, anti-SLC27A1, anti-GRIA, anti-OR4M1, anti-KIAA1679, or anti-UPK-1b
CC antibody, and a pharmaceutical carrier. The methods are useful for
CC detecting, diagnosing, and treating cancer, e.g. colon, lung, ovary,
CC prostate, pancreas, or bladder cancer. This is the amino acid sequence of
CC NGEP, altered levels of expression are useful in the diagnosis or
CC prognosis of cancer.
CC
CC Revised record issued on 18-OCT-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 933 AA;

Query Match 100.0%; Score 43; DB 11; Length 933;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ALLSASWAV 9
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Db        170 ALLSASWAV 178
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RESULT 7
ABJ01075

ID ABJ01075 standard; protein; 84 AA.
XX
AC ABJ01075;
XX
DT 28-NOV-2002 (first entry)
XX
DE Ovary cell-specific amino acid sequence 21.
XX
KW Ovary cell; neoplastic ovary cell; ovary specific nucleic acid;
KW ovary specific protein; ovarian cancer; breast cancer; vaccine;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO200238606-A2.
XX
PD 16-MAY-2002.
XX
PF 07-NOV-2001; 2001WO-US046459.
XX
PR 08-NOV-2000; 2000US-0246640P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Sun Y, Recipon H, Salceda S, Liu C;
XX
DR WPI; 2002-519297/55.
XX
PT Polypeptide and polynucleotides present in normal and neoplastic ovary
PT cells, useful for identifying, monitoring, staging, diagnosing,
PT preventing and treating ovarian cancer, and non-cancerous disease states
PT in the ovary.
XX
PS Claim 11; Page 214; 247pp; English.
XX
CC The invention comprises amino acid and DNA sequences which are present in
CC normal and neoplastic ovary cells. The DNA and protein sequences of the
CC invention are useful for determining the presence of an ovary specific
CC nucleic acid or an ovary specific protein in a sample. The DNA and
CC protein sequences of the invention are useful for diagnosing and
CC monitoring the presence and metastasis of ovarian cancer and breast
CC cancer. Amino acids ABJ01055 - ABJ01155 represent the ovary cell specific
CC protein sequences of the invention
XX
SQ Sequence 84 AA;

  Query Match   93.0%; Score 40; DB 5; Length 84;
  Best Local Similarity   88.9%; Pred. No. 24;
  Matches   8; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

```
Qy          1 ALLSASWAV 9
              :|||||||||
Db         64 SLLSASWAV 72
```

RESULT 8
AAB79567
ID   AAB79567 standard; protein; 113 AA.
XX
AC   AAB79567;
XX
DT   30-APR-2001 (first entry)
XX
DE   Corynebacterium glutamicum SMP protein sequence SEQ ID NO:650.
XX
KW   Corynebacterium glutamicum; carbon metabolism and energy production;
KW   SMP protein; sugar metabolism and oxidative phosphorylation protein;
KW   fine chemical production; organic acid; proteinogenic amino acid;
KW   nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
KW   nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
KW   carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
KW   diagnosis; Corynebacterium diphtheriae; evolutionary study.
XX
OS   Corynebacterium glutamicum.
XX
PN   WO200100844-A2.
XX
PD   04-JAN-2001.
XX
PF   23-JUN-2000; 2000WO-IB000943.
XX
PR   25-JUN-1999;   99US-0141031P.
PR   08-JUL-1999;   99DE-01031412.
PR   08-JUL-1999;   99DE-01031413.
PR   08-JUL-1999;   99DE-01031419.
PR   08-JUL-1999;   99DE-01031420.
PR   08-JUL-1999;   99DE-01031424.
PR   08-JUL-1999;   99DE-01031428.
PR   08-JUL-1999;   99DE-01031431.
PR   08-JUL-1999;   99DE-01031433.
PR   08-JUL-1999;   99DE-01031434.
PR   08-JUL-1999;   99DE-01031510.
PR   08-JUL-1999;   99DE-01031562.
PR   08-JUL-1999;   99DE-01031634.
PR   09-JUL-1999;   99DE-01032180.
PR   09-JUL-1999;   99DE-01032227.
PR   09-JUL-1999;   99DE-01032230.
PR   09-JUL-1999;   99US-0143208P.

PR 14-JUL-1999; 99DE-01032924.
PR 14-JUL-1999; 99DE-01032973.
PR 14-JUL-1999; 99DE-01033005.
PR 27-AUG-1999; 99DE-01040765.
PR 31-AUG-1999; 99US-0151572P.
PR 03-SEP-1999; 99DE-01042076.
PR 03-SEP-1999; 99DE-01042079.
PR 03-SEP-1999; 99DE-01042086.
PR 03-SEP-1999; 99DE-01042087.
PR 03-SEP-1999; 99DE-01042088.
PR 03-SEP-1999; 99DE-01042095.
PR 03-SEP-1999; 99DE-01042123.
PR 03-SEP-1999; 99DE-01042125.
XX
PA (BADI) BASF AG.
XX
PI Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;
XX
DR WPI; 2001-061975/07.
DR N-PSDB; AAF71684.
XX
PT New isolated Corynebacterium glutamicum nucleic acid encoding a sugar
PT metabolism and oxidative phosphorylation protein for production or
PT modulation of production of fine chemicals e.g. amino acids,
PT carbohydrates or enzymes.
XX
PS Claim 20; Page 1067; 1246pp; English.
XX
CC AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
CC metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243
CC to AAB 79633 which are involved in carbon metabolism and energy
CC production. The C. glutamicum SMP gene can be used in vectors (II) for
CC expression in host cells and production or modulation of production of
CC fine chemicals, such as, an organic acid, a proteinogenic or
CC nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a
CC nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid,
CC a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a
CC polyketide, or an enzyme. The presence of (I) or SMP proteins (III)
CC encoded by them are used for diagnosing the presence or activity of
CC Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells
CC containing them are used to map genomes of organisms related to C.
CC glutamicum, identify and localise C. glutamicum sequences of interest, in
CC evolutionary studies, in determining SMP protein regions required for
CC function, in modulating SMP protein activity, in modulating the
CC metabolism of sugars, and in modulating high-energy molecule production
CC in a cell (i.e. ATP, NADPH)
XX
SQ Sequence 113 AA;

```
  Query Match             88.4%;  Score 38;  DB 4;  Length 113;
  Best Local Similarity   77.8%;  Pred. No. 75;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ALLSASWAV 9
              |||| |||:
Db         88 ALLSGSWAI 96


RESULT 9
AAG90241
ID   AAG90241 standard; protein; 264 AA.
XX
AC   AAG90241;
XX
DT   15-JUN-2007  (revised)
DT   26-SEP-2001  (first entry)
XX
DE   C glutamicum protein fragment SEQ ID NO: 3995.
XX
KW   Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW   organic acid synthesis; BOND_PC; Cytochrome c biogenesis protein;
KW   Cytochrome c biogenesis protein [Corynebacterium glutamicum ATCC 13032].
XX
OS   Corynebacterium glutamicum.
XX
PN   EP1108790-A2.
XX
PD   20-JUN-2001.
XX
PF   18-DEC-2000; 2000EP-00127688.
XX
PR   16-DEC-1999;   99JP-00377484.
PR   07-APR-2000; 2000JP-00159162.
PR   03-AUG-2000; 2000JP-00280988.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Nakagawa S,  Mizoguchi H,  Ando S,  Hayashi M,  Ochiai K,  Yokoi H;
PI   Tateishi N,  Senoh A,  Ikeda M,  Ozaki A;
XX
DR   WPI; 2001-376931/40.
DR   N-PSDB; AAH65460.
DR   PC:NCBI; gi21323205.
XX
PT   Novel polynucleotides derived from Coryneform bacteria, for identifying
PT   mutation point of a gene, measuring expression of a gene, analyzing
PT   expression profile or pattern of a gene and identifying homologous gene.
XX
```

PS   Claim 17; SEQ ID NO 3995; 246pp + Sequence Listing; English.
XX
CC   The present invention provides a number of nucleotide and protein
CC   sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC   are useful for identifying the mutation point of a gene derived from a
CC   mutant of coryneform bacterium, measuring expression amount and analysing
CC   the expression profile or expression pattern of a gene derived from
CC   Coryneform bacterium, and identifying a homologue of a gene derived from
CC   coryneform bacterium. Coryneform bacteria are useful for producing amino
CC   acids, nucleic acids, vitamins, saccharides and organic acids,
CC   particularly L-lysine. The present sequence is a protein described in the
CC   exemplification of the invention. Note: The sequence data for this patent
CC   did not form part of the printed specification, but was obtained in
CC   electronic format directly from the European Patent Office
CC
CC   Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 264 AA;

  Query Match   88.4%; Score 38; DB 4; Length 264;
  Best Local Similarity   77.8%; Pred. No. 2e+02;
  Matches   7; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 ALLSASWAV 9
              |||| |||:
Db   239 ALLSGSWAI 247

RESULT 10
AEN26433
ID   AEN26433 standard; protein; 763 AA.
XX
AC   AEN26433;
XX
DT   22-FEB-2007 (first entry)
XX
DE   Oryza sativa stress tolerance protein - SEQ ID 11720.
XX
KW   transgenic plant; crop improvement; stress tolerance.
XX
OS   Oryza sativa.
XX
PN   US2005108791-A1.
XX
PD   19-MAY-2005.
XX
PF   10-DEC-2003; 2003US-00732923.
XX

PR 04-DEC-2001; 2001US-0337358P.
PR 04-DEC-2002; 2002US-00310154.
PR 22-FEB-2003; 2003US-0449054P.
XX
PA (EDGE/) EDGERTON M D.
XX
PI Edgerton MD;
XX
DR WPI; 2005-354826/36.
XX
PT New transgenic plant seed having a genome that comprises a recombinant
PT polynucleotide encoding S-adenosylmethionine decarboxylase or
PT deoxyhypusine synthase, useful for producing plants with enhanced yield.
XX
PS Claim 6; SEQ ID NO 11720; 29pp; English.
XX
CC The invention comprises a transgenic plant seed, where the genome of the
CC seed includes a recombinant polynucleotide encoding either an S-
CC adenosylmethionine decarboxylase or deoxyhypusine synthase enzyme, plants
CC grown from the seed exhibit enhanced yield. The seed of the invention is
CC useful for producing transgenic plants with enhanced phenotypes, such as
CC increased yield under environmental stress conditions. The present amino
CC acid sequence represents a protein that is useful for generating
CC transgenic plants with enhanced properties
XX
SQ Sequence 763 AA;

Query Match 83.7%; Score 36; DB 10; Length 763;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ALLSASWA 8
              |||||:||
Db        174 ALLSAAWA 181
```

RESULT 11
ADW81389
ID ADW81389 standard; protein; 869 AA.
XX
AC ADW81389;
XX
DT 07-APR-2005 (first entry)
XX
DE MAP3K9 genome derived polypeptide, MAP3K9.bDec03.
XX
KW mixed lineage kinase; MLK; asthma; at-risk haplotype; MAP3K9;
KW antiasthmatic; respiratory-gen.; antiinflammatory; antirheumatic;
KW antiarthritic; antipsoriatic; neuroprotective; gastrointestinal-gen.;

KW respiratory disease; chronic obstructive pulmonary disease;
KW chronic bronchitis; inflammation.
XX
OS Unidentified.
XX
PN WO2005007144-A2.
XX
PD 27-JAN-2005.
XX
PF 14-JUL-2004; 2004WO-US022446.
XX
PR 14-JUL-2003; 2003US-0487072P.
PR 05-APR-2004; 2004US-0559611P.
XX
PA (DECO-) DECODE GENETICS EHF.
XX
PI Hakonarson H, Gurney ME, Halapi E;
XX
DR WPI; 2005-122681/13.
DR N-PSDB; ADW81384.
XX
PT Use of mixed lineage kinase family kinase inhibitor in the manufacture of
PT a medicament for treatment of asthma associated at-risk haplotype for
PT asthma, at-risk haplotype in MAP3K9 gene or increased MLK1 protein
PT expression or activity.
XX
PS Disclosure; Fig 11; 640pp; English.
XX
CC The invention relates to the novel use of a mixed lineage kinase (MLK)
CC family kinase inhibitor for treating asthma. Where the asthma is
CC associated with a risk factor selected from an at-risk haplotype for
CC asthma, at-risk haplotype in MAP3K9 gene, polymorphism in MAP3K9 nucleic
CC acid, dysregulation of MAP3K9 mRNA expression, dysregulation of a MAP3K9
CC mRNA isoform, and/or increased MLK1 protein expression. The invention
CC further comprises: a method for the diagnosis or identification of
CC susceptibility to asthma; a method for the use of a first nucleic acid
CC molecule for diagnosing asthma or susceptibility to asthma in a sample; a
CC method for assaying the presence of a first nucleic acid molecule in a
CC sample; a method for assessing the response to treatment with an MLK
CC family kinase nucleic acid inhibitor in a target population or in an
CC individual with an at-risk haplotype for asthma, at-risk haplotype in the
CC MAP3K9 gene, polymorphism in the MAP3K9 nucleic acid, dysregulation of
CC MAP3K9 mRNA expression, dysregulation of MAP3K9 mRNA isoform, increased
CC MLK1 protein expression, increased MLK1 biochemical activity or increased
CC MLK1 protein isoform expression; a method for assessing the response to
CC treatment with an MLK1 inhibitor in a target population including an
CC individual with an at-risk haplotype for asthma, as above; a kit for
CC assaying a sample for the presence or absence of at least one haplotype
CC comprising 2 or more alleles associated with asthma comprising: at least

CC one nucleic acid capable of detecting the presence or absence of at least
CC one specific allele; a reagent kit for assaying the presence of at least
CC one haplotype comprising 2 or more alleles comprising: at least one
CC labeled nucleic acid capable of detecting at least one specific allele of
CC the haplotype, and reagents for detection of the label; and a reagent kit
CC for assaying a sample for the presence of at least one haplotype
CC comprising 2 or more alleles comprising: at least one nucleic acid
CC comprising at least one nucleotide sequence that is at least partially
CC complementary to a part of nucleotide sequence of MAP3K9, capable of
CC acting as a primer for a primer extension reaction and capable of
CC detecting 2 or more specific alleles of the haplotype. The MLK family
CC kinase inhibitor has the following activities: antiasthmatic, respiratory
CC -gen., antiinflammatory, antirheumatic, antiarthritic, antipsoriatic,
CC neuroprotective, and gastrointestinal-gen. The MLK family kinase
CC inhibitor is useful for the treatment of asthma associated with a risk
CC factor selected from at-risk haplotype for asthma, at-risk haplotype in
CC MAP3K9 gene, polymorphism in MAP3K9 nucleic acid, dysregulation of MAP3K9
CC mRNA expression, dysregulation of MAP3K9 mRNA isoform, increased MLK1
CC protein expression, increased MLK1 biochemical activity and/or increased
CC MLK1 protein isoform expression; and in diagnosis or identification of
CC susceptibility to asthma. The inhibitor is also useful for the treatment
CC of other respiratory diseases associated with MAP3K9 or other members of
CC the JNK pathway such as chronic obstructive pulmonary disease, chronic
CC bronchitis and other inflammatory diseases such as rheumatoid arthritis,
CC psoriasis, multiple sclerosis and inflammatory bowel disease. This
CC sequence represents a polypeptide derived from the genomic DNA of the
CC MAP3K9 kinase protein, where MAP3K9 is a part of Mitogen-Activated
CC Protein Kinase (MAPK) signal transduction pathways, of the invention.
XX
SQ Sequence 869 AA;

Query Match 83.7%; Score 36; DB 10; Length 869;
Best Local Similarity 77.8%; Pred. No. 1.7e+03;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 ALLSASWAV 9
              |||:||| |
Db        427 ALLAASWVV 435
```

RESULT 12
AEK84872
ID AEK84872 standard; protein; 869 AA.
XX
AC AEK84872;
XX
DT 28-DEC-2006 (first entry)
XX
DE Human MAP3K9/MLK1 cDNA splice variant b, protein.

XX
KW Haplotype mapping; DNA typing; diagnosis; SNP detection; polymorphism;
KW enzyme; MAP3K9; MLK1; mixed lineage kinase;
KW mitogen activated protein kinase; pharmaceutical; therapeutic; asthma;
KW allergic rhinitis; atopic eczema; antiasthmatic; immune disorder;
KW inflammation; respiratory disease; antiallergic; antiinflammatory;
KW ear, nose, throat disease; dermatological; dermatological disease;
KW splice variant.
XX
OS Homo sapiens.
XX
PN WO2006081555-A2.
XX
PD 03-AUG-2006.
XX
PF 26-JAN-2006; 2006WO-US003220.
XX
PR 26-JAN-2005; 2005US-00043752.
XX
PA (DECO-) DECODE GENETICS EHF.
XX
PI Hakonarson H, Gurney M, Halapi E;
XX
DR WPI; 2006-797726/81.
DR N-PSDB; AEK84867.
XX
PT Use of mixed lineage kinase family kinase inhibitor for manufacture of
PT medicament for treatment for allergic rhinitis in individual with at-risk
PT haplotype for allergic rhinitis, in MAP3K9 gene.
XX
PS Disclosure; SEQ ID NO 45; 1337pp; English.
XX
CC The invention relates to a medicament manufacturing method for treating
CC e.g. asthma, involves detecting presence/absence of nucleic acid molecule
CC of a marker of an at-risk haplotype (mixed lineage kinase (MLK) family
CC kinase 1, also knownn as MAP3K9), and administering inhibitor to
CC individual in therapeutically effective amount. Also included is a
CC reagent kit for assaying a sample for presence of haplotype associated
CC with allergic rhinitis. The method is used for manufacturing a medicament
CC to treat asthma and allergic rhinitis in a person. The method administers
CC mixed lineage kinase (MLK) family kinase inhibitor to the individual in
CC the therapeutically effective amount, thus diagnosing a predisposition to
CC the asthma, allergic rhinitis, and atopic eczema and treating the people
CC who have the asthma, allergic rhinitis and atopic eczema in an efficient
CC manner. The gene for human MLK1 is located at chromosome 14q24. The
CC present sequence represents the human MLK1/MAP3K9 protein encoded by a
CC cDNA splice variant.
XX
SQ Sequence 869 AA;

```
  Query Match             83.7%;  Score 36;  DB 11;  Length 869;
  Best Local Similarity   77.8%;  Pred. No. 1.7e+03;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ALLSASWAV 9
              |||:||| |
Db        427 ALLAASWVV 435


RESULT 13
ADO01052
ID   ADO01052 standard; protein; 922 AA.
XX
AC   ADO01052;
XX
DT   15-JUN-2007  (revised)
DT   01-JUL-2004  (first entry)
XX
DE   Human homologue of Fruit fly AD-related protein CG8789 #6.
XX
KW   Human; Alzheimer's disease; Gamma secretase; Psn gene; P-element; EP;
KW   APPL-SV; Amyloid precursor-like protein; APP;
KW   suppressor of hairless transcription factor; Su(H);
KW   VP16 activation domain; dementia; memory loss; language deterioration;
KW   impaired visuospatial skill; BOND_PC;
KW   mitogen-activated protein kinase kinase kinase 9, isoform CRA_b; GO166;
KW   GO4674; GO4706; GO4708; GO4713; GO5524; GO5575; GO7257; GO16740; GO42803;
KW   GO46777.
XX
OS   Homo sapiens.
XX
PN   US2004067535-A1.
XX
PD   08-APR-2004.
XX
PF   03-OCT-2002; 2002US-00263929.
XX
PR   03-OCT-2002; 2002US-00263929.
XX
PA   (LIFE-) LIFE SCI DEV CORP.
XX
PI   Kim J,  Galant R;
XX
DR   WPI; 2004-355296/33.
DR   N-PSDB; ADO00950.
DR   PC:NCBI; gi119601452.
XX
PT   Identifying compound by exposing cell that expresses gene having
```

PT enhancing or suppression effect on APPL-SV phenotype to agent,
PT identifying modulation of Alzheimer's disease (AD), regulation of gene or
PT protein expression with AD.
XX
PS Claim 18; SEQ ID NO 190; 185pp; English.
XX
CC The invention relates to identifying a compound comprising exposing cell
CC expressing gene 1 having enhancing or suppression effect on an APPL-SV
CC phenotype (a transgenic fruit fly expressing the Amyloid precursor-like
CC protein, APP, as a fusion protein with the suppressor of hairless
CC transcription factor , Su(H) and VP16 activation domain. The fusion
CC protein is cleaved by gamma secretase (encoded by the Psn gene) to
CC release the Su(H-VP16, which affects wing vein development. Genes
CC affecting Psn expression/activity were screened by crossing the APP-SV
CC line with an EP P-element insertion library, and the DNA recovered from
CC the appropriate EP strain and sequenced) chosen from ADO00863-ADO00964,
CC being the identified fruit fly genes affecting APP processing and their
CC mammalian homologues, identifying modulation of Alzheimer's disease (AD)
CC symptom, regulation of biological pathway, gene expression or protein
CC function associated with AD relative to cell in absence of agent. Also
CC included are regulating AD (involves providing a subject with AD or
CC symptoms of AD and an agent that changes the expression of a gene
CC detailed above or changes the activity of a polypeptide having a sequence
CC chosen from ADO00965-ADO01066, and treating the subject with the agent)
CC and a composition (comprising a nucleic acid encoding a polypeptide
CC detailed above or an expression vector comprising the nucleic acid or a
CC host cell comprising the expression vector or an antisense
CC oligonucleotide that hybridises under stringent conditions to the nucleic
CC acid or polypeptide or an antibody that specifically binds to the
CC polypeptide). The method is useful for identifying compounds modulating
CC symptom of Alzheimer's disease (AD), regulation of biological pathway
CC associated with AD, or regulation of gene expression or protein function
CC of gene or protein associated with AD. The nucleic acids and proteins are
CC useful in drug screening and useful in screening and treating the subject
CC having increased susceptibility to AD or symptoms of AD such as dementia,
CC memory loss, language deterioration and impaired visuospatial skills. The
CC present sequence is a human homologue of a fruit fly protein from a gene
CC identified as having an effect on the APP-SV phenotype.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 922 AA;

Query Match 83.7%; Score 36; DB 8; Length 922;
Best Local Similarity 77.8%; Pred. No. 1.8e+03;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ALLSASWAV 9

```
              |||:||| |
Db        480 ALLAASWVV 488


RESULT 14
AEN28397
ID   AEN28397 standard; protein; 1066 AA.
XX
AC   AEN28397;
XX
DT   22-FEB-2007  (first entry)
XX
DE   Homo sapiens stress tolerance protein - SEQ ID 13684.
XX
KW   transgenic plant; crop improvement; stress tolerance.
XX
OS   Homo sapiens.
XX
PN   US2005108791-A1.
XX
PD   19-MAY-2005.
XX
PF   10-DEC-2003; 2003US-00732923.
XX
PR   04-DEC-2001; 2001US-0337358P.
PR   04-DEC-2002; 2002US-00310154.
PR   22-FEB-2003; 2003US-0449054P.
XX
PA   (EDGE/) EDGERTON M D.
XX
PI   Edgerton MD;
XX
DR   WPI; 2005-354826/36.
XX
PT   New transgenic plant seed having a genome that comprises a recombinant
PT   polynucleotide encoding S-adenosylmethionine decarboxylase or
PT   deoxyhypusine synthase, useful for producing plants with enhanced yield.
XX
PS   Claim 6; SEQ ID NO 13684; 29pp; English.
XX
CC   The invention comprises a transgenic plant seed, where the genome of the
CC   seed includes a recombinant polynucleotide encoding either an S-
CC   adenosylmethionine decarboxylase or deoxyhypusine synthase enzyme, plants
CC   grown from the seed exhibit enhanced yield. The seed of the invention is
CC   useful for producing transgenic plants with enhanced phenotypes, such as
CC   increased yield under environmental stress conditions. The present amino
CC   acid sequence represents a protein that is useful for generating
CC   transgenic plants with enhanced properties
XX
```

```
SQ   Sequence 1066 AA;

  Query Match             83.7%;  Score 36;  DB 10;  Length 1066;
  Best Local Similarity   77.8%;  Pred. No. 2.1e+03;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ALLSASWAV 9
              |||:||| |
Db        624 ALLAASWVV 632



RESULT 15
ADW81388
ID   ADW81388 standard; protein; 1071 AA.
XX
AC   ADW81388;
XX
DT   07-APR-2005  (first entry)
XX
DE   MAP3K9 genome derived polypeptide, MAP3K9.aDec03.
XX
KW   mixed lineage kinase; MLK; asthma; at-risk haplotype; MAP3K9;
KW   antiasthmatic; respiratory-gen.; antiinflammatory; antirheumatic;
KW   antiarthritic; antipsoriatic; neuroprotective; gastrointestinal-gen.;
KW   respiratory disease; chronic obstructive pulmonary disease;
KW   chronic bronchitis; inflammation.
XX
OS   Unidentified.
XX
PN   WO2005007144-A2.
XX
PD   27-JAN-2005.
XX
PF   14-JUL-2004; 2004WO-US022446.
XX
PR   14-JUL-2003; 2003US-0487072P.
PR   05-APR-2004; 2004US-0559611P.
XX
PA   (DECO-) DECODE GENETICS EHF.
XX
PI   Hakonarson H,  Gurney ME,  Halapi E;
XX
DR   WPI; 2005-122681/13.
DR   N-PSDB; ADW81383.
XX
PT   Use of mixed lineage kinase family kinase inhibitor in the manufacture of
PT   a medicament for treatment of asthma associated at-risk haplotype for
PT   asthma, at-risk haplotype in MAP3K9 gene or increased MLK1 protein
PT   expression or activity.
```

XX
PS Disclosure; Fig 11; 640pp; English.
XX
CC The invention relates to the novel use of a mixed lineage kinase (MLK)
CC family kinase inhibitor for treating asthma. Where the asthma is
CC associated with a risk factor selected from an at-risk haplotype for
CC asthma, at-risk haplotype in MAP3K9 gene, polymorphism in MAP3K9 nucleic
CC acid, dysregulation of MAP3K9 mRNA expression, dysregulation of a MAP3K9
CC mRNA isoform, and/or increased MLK1 protein expression. The invention
CC further comprises: a method for the diagnosis or identification of
CC susceptibility to asthma; a method for the use of a first nucleic acid
CC molecule for diagnosing asthma or susceptibility to asthma in a sample; a
CC method for assaying the presence of a first nucleic acid molecule in a
CC sample; a method for assessing the response to treatment with an MLK
CC family kinase nucleic acid inhibitor in a target population or in an
CC individual with an at-risk haplotype for asthma, at-risk haplotype in the
CC MAP3K9 gene, polymorphism in the MAP3K9 nucleic acid, dysregulation of
CC MAP3K9 mRNA expression, dysregulation of MAP3K9 mRNA isoform, increased
CC MLK1 protein expression, increased MLK1 biochemical activity or increased
CC MLK1 protein isoform expression; a method for assessing the response to
CC treatment with an MLK1 inhibitor in a target population including an
CC individual with an at-risk haplotype for asthma, as above; a kit for
CC assaying a sample for the presence or absence of at least one haplotype
CC comprising 2 or more alleles associated with asthma comprising: at least
CC one nucleic acid capable of detecting the presence or absence of at least
CC one specific allele; a reagent kit for assaying the presence of at least
CC one haplotype comprising 2 or more alleles comprising: at least one
CC labeled nucleic acid capable of detecting at least one specific allele of
CC the haplotype, and reagents for detection of the label; and a reagent kit
CC for assaying a sample for the presence of at least one haplotype
CC comprising 2 or more alleles comprising: at least one nucleic acid
CC comprising at least one nucleotide sequence that is at least partially
CC complementary to a part of nucleotide sequence of MAP3K9, capable of
CC acting as a primer for a primer extension reaction and capable of
CC detecting 2 or more specific alleles of the haplotype. The MLK family
CC kinase inhibitor has the following activities: antiasthmatic, respiratory
CC -gen., antiinflammatory, antirheumatic, antiarthritic, antipsoriatic,
CC neuroprotective, and gastrointestinal-gen. The MLK family kinase
CC inhibitor is useful for the treatment of asthma associated with a risk
CC factor selected from at-risk haplotype for asthma, at-risk haplotype in
CC MAP3K9 gene, polymorphism in MAP3K9 nucleic acid, dysregulation of MAP3K9
CC mRNA expression, dysregulation of MAP3K9 mRNA isoform, increased MLK1
CC protein expression, increased MLK1 biochemical activity and/or increased
CC MLK1 protein isoform expression; and in diagnosis or identification of
CC susceptibility to asthma. The inhibitor is also useful for the treatment
CC of other respiratory diseases associated with MAP3K9 or other members of
CC the JNK pathway such as chronic obstructive pulmonary disease, chronic
CC bronchitis and other inflammatory diseases such as rheumatoid arthritis,
CC psoriasis, multiple sclerosis and inflammatory bowel disease. This

CC sequence represents a polypeptide derived from the genomic DNA of the
CC MAP3K9 kinase protein, where MAP3K9 is a part of Mitogen-Activated
CC Protein Kinase (MAPK) signal transduction pathways, of the invention.
XX
SQ Sequence 1071 AA;

Query Match 83.7%; Score 36; DB 10; Length 1071;
Best Local Similarity 77.8%; Pred. No. 2.2e+03;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ALLSASWAV 9
              |||:||| |
Db        629 ALLAASWVV 637
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Search completed: June 30, 2008, 17:52:55
Job time : 76.875 secs